
SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Yelton, Dale E.
Rosok, Mae Joanne

(ii) TITLE OF THE INVENTION: A METHOD FOR INHIBITING IMMUNOGLOBULIN-INDUCED TOXICITY RESULTING FROM THE USE OF IMMUNOGLOBULINS IN THERAPY AND IN VIVO DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
- (B) STREET: 11150 Santa Monica Boulevard, Suite 400
- (C) CITY: Los Angeles
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 90025

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/905,293
- (B) FILING DATE: 01-AUG-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/023,033
- (B) FILING DATE: 02-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Canady, Karen S
- (B) REGISTRATION NUMBER: 39,927
- (C) REFERENCE/DOCKET NUMBER: 30436.43USU1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 310-445-1140
- (B) TELEFAX: 310-445-9031
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGCACCGAA AGCTTTCTGG GGCAGGCCAG GCCTGA

36

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCGGACATG TTGGTACCCA CGTGGTGGTC GACGCTGAGC CTGGCTTCGA GCAGACA

57

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACCACC ACGTGGGTAC CAACATGTCC GGAGGCCACAT GGACAGAGGC CGGCT

55

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGTTCTTG GTCATCTCCT CTCTAGATGG

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCATGGTCG ACCTCAGACC TGCCAAGAGC CATATC

36

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATGGTCACG TGGTGTGTCC CTGGATGCAG GCTACTCTAG

40

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGGAGGGGA GGGTGTCTGC TGGAAGCCAG GCTCAGCGCT GACCTCAGA

49

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGAAAGAACC ATCACAGTCT CGCAGGGGCC CAGGGCAGCG CTGGGTGCTT

50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACGGATCGG GAGATCTGCT AGGTGACCTG AGGCGCGCCG GCTTCGAATA GCCAGAGTAA
CCTTTTTTTT TAATTTTATT TTATTTTATT TTTGAGATGG AGTTTGGCGC CGATCTCCCG
ATCCCCCTATG GTCGACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAGTATC
TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGCAG GAGCAAATT TAAGCTACAA
CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT TAGGGTTAGG CGTTTGCAG

60

120

180

240

300

TGCTTCGCGA	TGTACGGGCC	AGATATAACGC	GTTGACATTG	ATTATTGACT	AGTTATTAAT	360
AGTAATCAAT	TACGGGGTCA	TTAGTTCAT	GCCCATAAT	GGAGTCCGC	GTTACATAAC	420
TTACGGTAA	TGGCCCGCCT	GGCTGACC	CCAACGACCC	CCGCCCCATTG	ACGTCAATAA	480
TGACGTATGT	TCCCATA	ACGCCAATAG	GGACTTCCA	TTGACGTCAA	TGGGTGGACT	540
ATTTACGGTA	AACTGCCAC	TTGGCAGTAC	ATCAAGTGT	TCATATGCCA	AGTACGCC	600
CTATTGACGT	CAATGACGGT	AAATGGCCG	CCTGGCATT	TGCCCAGTAC	ATGACCTTAT	660
GGGACTTCC	TACTTGGCAG	TACATCTACG	TATTAGTCAT	CGCTATTACC	ATGGTGATGC	720
GGTTTGGCA	GTACATCAAT	GGCGTGGAT	AGCGGTTGA	CTCACGGGGA	TTTCCAAGTC	780
TCCACCCAT	TGACGTCAA	GGGAGTTGT	TTTGGCACCA	AAATCAACGG	GACTTICCAA	840
AATGTCGAA	CAACTCCGCC	CCATTGACGC	AAATGGCGG	TAGGCGTGT	CGGTGGGAGG	900
TCTATATAAG	CAGAGCTCTC	TGGCTAACTA	GAGAACCCAC	TGCTTACTGG	CTTATCGAAA	960
TTAATACGAC	TCACTATAGG	GAGACCAAG	CTTGGTACCA	ATTTAAATTG	ATATCTCCTT	1020
AGGTCTCGAG	TCTCTAGATA	ACCGGTCAT	CGATTGGAAT	TCTTGC	GCTTGCTAGC	1080
CACCATGGAG	TTGTGGTTAA	GCTTGGTCCT	TCCTTGT	TGTTTAAAAA	GGTGTCCAGT	1140
GTGAAGTGAA	TCTGGTGGAG	TCTGGGGAG	GCTTAGTGCA	GCCTGGAGGG	TCCCTGAAAG	1200
TCTCCTGTGT	AAACCTCTGGA	TTCACTTCA	GTGACTATT	CATGTATTG	GTTGCCAGA	1260
CTCCAGAGAA	GAGGCTGGAG	TGGGTCGAT	ACATTAGTCA	AGGTGGTGT	ATAACCGACT	1320
ATCCAGACAC	TGTAAAGGGT	CGATTCA	TCTCCAGAGA	CAATGCCAAG	AAACCCCTGT	1380
ACCTGCAAAT	GAGCCGCTG	AAAGTCTGAGG	ACACAGCCAT	GTATTACTGT	GCAAGAGGCC	1440
TGGACGACGG	GGCCTGGTTT	GCTTACTGGG	GCCAAGGGAC	TCTGGTCACG	GTCTCTGTAG	1500
CTAGCACAA	GGGCCATCG	GTCTTCCCC	TGGCACCC	CTCCAAGAGC	ACCTCTGGG	1560
GCACAGGGC	CCTGGGCTGC	CTGGTCAAGG	ACTACTCCC	CGAACCGGTG	ACGGTGT	1620
GGAACCTCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTCCC	GGCTGTCTA	CAGTCCTCAG	1680
GACTCTACTC	CCTCAGCAGC	GTGGTCACCG	TGCCCCTCAG	CAGCTGGGC	ACCCAGACCT	1740
ACATCTGAA	CGTAAATCA	AAGCCAGCA	ACACCAAGGT	GGACAAGAAA	GTTGGT	1800
GGCCAGCACA	GGGAGGGAGG	GTGTCTGCTG	GAAGCCAGGC	TCAGCGCTCC	TGCTGGACG	1860
CATCCCCGCT	ATGCAGCCCC	AGTCCAGGGC	AGCAAGGAG	GCCCCGCT	CCTCTTCACC	1920
CGGAGGCC	TGCCCCCCCC	ACTCATGCTC	AGGGAGAGGG	TCTTCTGGCT	TTTCCCCAG	1980
GCTCTGGCA	GGCACAGGCT	AGGTGCCCT	AACCCAGGCC	CTGGCACACAA	AGGGCAGGT	2040
GCTGGGCTCA	GACCTGCCA	GAGCCATATC	CGGGAGGACC	CTGCCCCTGA	CCTAAGGCCA	2100
CCCCAAAGGC	CAAACCTCTC	ACTCCCTCAG	CTCGACACC	TTCTCTCCTC	CCAGATTCCA	2160
GTAACTCCC	ATCTCTCTC	TGCAGAGCC	AAATTTGTG	ACAAAAC	TCACATGCCA	2220
CCGTGCCAG	GTAAGCCAGC	CCAGGCC	CCCTCCAGCT	CAAGGGGGG	CAGGTGCC	2280
AGAGTAGCCT	GCATCCAGGG	ACAGGCCCA	GCCGGGTGCT	GACACGT	CCTCCATCTC	2340
TTCCCTCAGCA	CCTGA	CTGGGGGACC	GTCAGTCTTC	CTCTCTCCC	CAAACCCAA	2400
GGACACCCCT	ATGATCTCC	GGACCCCTGA	GGTCACATGC	GTGGTGTG	ACGTGAGCCA	2460
CGAAGACCC	GAGGTCAAGT	TCAACTGGT	CGTGGACGGC	GTGGAGGTG	ATAATGCCA	2520
GACAAAGCCG	CGGGAGGAGC	AGTACAACAG	CACGTACCGT	GTGGTCAGCG	TCCTCACCGT	2580
CCTGCACCAG	GACTGGCTGA	ATGGCAAGGA	GTACAAGTGC	AAGGTCTCCA	ACAAAGCCCT	2640
CCCAGCCCC	ATCGAGAAAA	CCATCTCCAA	AGCCAAAGGT	GGGACCCGTG	GGGTGCGAGG	2700
GCCACATGGA	CAGAGGCC	CTCGGCCAC	CCTCTGCC	GAGAGT	GACCT	2760
CCTCTGTCCC	TACAGGGCAG	CCCCGAGAAC	CACAGGTG	CACCCCTGCC	CCATCCC	2820
ATGAGCTGAC	CAAGAACCG	GTCAGCTGA	CCTGCC	TGAGGCTTC	TATCCCAGCG	2880
ACATGCCGT	GGAGTGGGAG	AGCAATGGC	AGCCGGAGA	CAACTACAAG	ACCACGCC	2940
CCGTGCTGGA	CTCCGACGGC	TCCTTCTTCC	TCTACAGCA	GTCACCGT	GACAAGAGCA	3000
GGTGGCAGCA	GGGGAACGTC	TTCTCATGCT	CCGTGATGCA	TGAGGCT	CACAACCA	3060
ACACGCAGAA	GAGCCTCTCC	CTGTCTCCG	GTAAATGAGT	GCGACGGCC	GCAAGCCCC	3120
GCTCCCCGG	CTCTCGCGGT	CGCACGAGGA	TGCTTGGC	GTACCCCTG	TACATACTC	3180
CCGGGCGCC	AGCATGGAAA	TAAAGCACCC	AGCGT	GGCC	CGAGACTGTG	3240
ATGGTTCTT	CCACGGGTCA	GGCCGAGTCT	GAGGCTGAG	TGGCATGAGG	GAGGCAGAGC	3300
GGGTCCCAC	GTCCCCACAC	TGGCC	TGTGAGGTG	TGCCTGGG	CCCTAGGTG	3360
GGGCTCAGCC	AGGGGCTGCC	CTCGCAGGG	TGGGG	GCCAGCGT	CCCTCC	3420
AGCAGCACCT	GCCTGGGCT	GGGCCACGG	AAGCCTAGG	AGCCCCTGG	GACAGACAC	3480
CAGCCCC	CTCTGTAGGA	GACTGCTCTG	TTCTGTGAGC	GCCCC	TCCCGACCTC	3540
CATGCCCA	CGGGGGCATG	CCTAGTCCAT	GTGCGTAGGG	ACAGGCC	CCTCACCC	3600
CTACCCCCAC	GGCACTAAC	CCTGGCTGCC	CTGCC	TCGCACCC	ATGGGACAC	3660
AACCGACTCC	GGGGACATGC	ACTCTGGGC	CCTGTGGAGG	GACTGGT	GATGCC	3720
CACACACTCA	GCCCAGACCC	GTTCAACAA	CCCCGACTG	AGGTTGGC	GCCACACGG	3780
ACCCACACAC	ACACGTGCAC	GCCTCACACA	CGGAGCCTCA	CCC	CTGCACAGCA	3840
CCCAGACCA	AGCAAGGTCC	TCGACACAGT	GAACACTCCT	CGGACACAGG	CCCCACGAG	3900

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CCCCACGGCGG	CACCTCAAGG	CCCACGAGCC	TCTCGGCAGC	TTCTCCACAT	GCTGACCTGC	3960
TCAGACAAAC	CCAGCCCTCC	TCTCACAAAGG	GTGCCCTCTGC	AGCCGCCACA	CACACACAGG	4020
GGATCACACA	CCACGTCACG	TCCCTGGCCC	TGGCCCACCTT	CCCAGTGCAGG	CCCTCCCTG	4080
CAGGACGGAT	CAGCCTCGAC	TGTGCCTCT	AGTTGCCAGC	CATCTGTTGT	TTGCCCTCC	4140
CCCGTGCCTT	CCTTGACCCCT	GGAAAGGTGCC	ACTCCCACGT	TCCTTCTCTA	ATAAAATGAG	4200
GAAATTGCAT	CGCATTGTC	GAGTAGGTGT	CATTCTATTTC	TGGGGGGTGG	GGTGGGGCAG	4260
GACAGCAAGG	GGGAGGATTG	GGAAAGACAAT	AGCAGGCATG	CTGGGGATGC	GGTGGGCTCT	4320
ATGGCTCTG	AGGCGGAAAG	AACCAGCTGG	GGCTCTAGGG	GGTATCCCCA	CGGCCCTGT	4380
AGCGGGCGAT	TAAGCGCGGC	GGGTGTGGTG	GTTACCGCGA	GCGTGACCAG	TACACTGCC	4440
AGCGCCCTAG	CGCCCCGCTCC	TTTCGCTTTC	TTCCCTTCCT	TTCTCGCCAC	GTTCGCCGGG	4500
CCTCTCAAAA	AAGGGAAAAAA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCAGCC	4560
CTAACCTCGC	CCATCCCGCC	CCTAACCTCG	CCCAGTTCCG	CCCATTCTCC	GCCCCATGGC	4620
TGACTAATTT	TTTTTATTTA	TGCAAGAGGC	GAGGCCGCCT	GGGCCTCTGA	GCTATTCCAG	4680
AAGTAGTGAG	GAGGGTTTTT	TGGAGGCCTA	GGCTTTGCA	AAAAGCTTGG	ACAGCTCAGG	4740
GCTGCGATTT	CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTATC	4800
CCCGCTGCCA	TCATGGTTCG	ACCATTGAAC	TGCACTCGTG	CCGTGTCCCA	AAATATGGG	4860
ATTGGCAAGA	ACGGAGACCT	ACCCCTGGCT	CCGCTCAGGA	ACGAGTTCAA	GTACTTCAA	4920
AGAATGACCA	CAACCTCTTC	AGTGGAAAGT	AAACAGAACAT	TGGTGATTAT	GGGTAGGAAA	4980
ACCTGGTTCT	CCATTCCCTGA	GAAGAACATGA	CCTTAAAGG	ACAGAATTAA	TATAGTTCTC	5040
AGTAGAGAAC	TCAAGAACACC	ACCACGAGGA	GCTCATTTC	TTGCCAAAG	TTTGGATGAT	5100
GCCTTAAGAC	TTATTGAACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAGTC	5160
GGAGGCAGTT	CTGTTTACCA	GGAAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTGTG	5220
ACAAGGATCA	TGCAAGAACATT	TGAAAGTGCAC	ACGTTTTCC	CAGAAATTGA	TTTGGGGAAA	5280
TATAAACTTC	TCCCAGAATA	CCCAGCGTC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	5340
AAGTATAAGT	TTGAAGTCTA	CGAGAAGAAA	GACTAACAGG	AAAGATGCTT	CAAGTTCTCT	5400
GCTCCCCCTCC	TAAAGCTATG	CATTTTTATA	AGACCATGGG	ACTTTGCTG	GCTTTAGATC	5460
TCTTTGTGAA	GGAACCTTAC	TTCTGTGGTG	TGACATAATT	GGACAAACTA	CCTACAGAGA	5520
TTTAAAGCTC	TAAGGTAAAT	ATAAAATTT	TAAGTGTATA	ATGTGTTAA	CTACTGATT	5580
TAATTGTTG	TGTATTTC	ATTCCAACCT	ATGGAACACTGA	TGAATGGGAG	CAGTGGTGGA	5640
ATGCCTTAA	TGAGGAAAC	CTGTTTGCT	CAGAAGAAAT	GCCATCTAGT	GATGATGAGG	5700
CTACTGCTGA	CTCTCAACAT	TCTACTCCTC	CAAAAAAGAA	GAGAAAGGTA	GAAGACCCCA	5760
AGGACTTTCC	TTCAGAACATTG	CTAAGTTTT	TGAGTCATGC	TGTGTTAGT	AATAGAACTC	5820
TTGCTTGCTT	TGCTATTTC	ACCACAAAGG	AAAAGCTGC	ACTGCTATAC	AAGAAAATTA	5880
TGGAAAAATA	TTCTGTAACC	TTTATAAGTA	GGCATAACAG	TTATAATCAT	AACATACTGT	5940
TTTTCTTAC	TCCACACAGG	CATAGAGTGT	CTGCTATTAA	TAACATATGCT	CAAAAATTGT	6000
GTACCTTAG	CTTTTTAATT	TGTAAGGGG	TTAATAAGGA	ATATTTGATG	TATAGTGCCT	6060
TGACTAGAGA	TCATAATCAG	CCATACACAA	TTTGTAGAGG	TTTACTTGC	TTIAAAAAC	6120
CTCCCCACACC	TCCCCCTGAA	CCTGAAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACCTTG	6180
TTTATTGCA	CTTATAATGG	TTACAAATAA	AGCAATAGCA	TCACAAATT	CACAAATAAA	6240
GCATTTTTT	CACTGCATTC	TAGTTGTTG	TTGTCACAAAC	TCATCAATGT	ATCTTATCAT	6300
GTCTGGATCG	GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	TGCTGGAGTT	CTTCGCCAC	6360
CCCAACTTGT	TTATTGCA	TTATAATGGT	TACAAATAAA	GCAATAGCAT	CACAAATTTC	6420
ACAAATAAAG	CATTTTTTC	ACTGCATTCT	AGTTGTTGGT	TGTCCAAACT	CATCAATGTA	6480
TCTTATCATG	TCTGTATACC	GTCGACCTCT	AGCTAGAGCT	TGGCGTAATC	ATGGTCATAG	6540
CTGTTTCTG	TGTAAATTG	TTATCCGTC	ACAATTCCAC	ACAACATAG	AGCCGGAAGC	6600
ATAAAAGTGA	AAGCTGGGG	TGCCTAATGA	GTGAGCTAAC	TCACATTAAT	TGCGTTGCGC	6660
TCACTGCCCG	CTTTCCAGTC	GGGAAACCTG	TCGTGCCAGC	TGCAATTAA	AATCGGCCAA	6720
CGCGCGGGGA	GAGGGGGTTT	GCGTATTGGG	CGCTCTTCG	CTTCCTCGCT	CACTGACTCG	6780
CTGCGCTCGG	TCGTTGGCT	GCGCGAGCG	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	6840
TTATCCACAG	AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGAAAAGG	CCAGCAAAG	6900
GCCAGGAACC	GTAAAAAGGC	CGCGTTGCTG	CGCTTTTCC	ATAGGCTCCG	CCCCCTGAC	6960
GAGCATCACA	AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	7020
TACCAGGCGT	TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	7080
ACCGGATACC	TGTCCGCTT	TCTCCCTTCG	GGAAGCGTGG	CGCTTTCTCA	ATGCTCACGC	7140
TGTAGGTATC	TCAGTTCGGT	GTAGGTGCTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	7200
CCCGTTCAGC	CCGACCGCTG	CGCCTTATCC	GGTAACTATC	GTCTTGAGTC	CAACCCGGTA	7260
AGACACGACT	TATGCCACT	GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	7320
GTAGGGCGTG	CTACAGAGTT	CTTGAAGTGG	TGGCTTA	ACGGCTACAC	TAGAAGGACA	7380
GTATTTGGTA	TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	AAAAAAGAGT	TGGTAGCTCT	7440
TGATCCGGCA	AAACAAACCAC	CGCTGGTAGC	GGTGGTTTTT	TTGTTGCAA	GCAGCAGATT	7500

ACGCGCAGAA	AAAAAGGATC	TCAAGAAGAT	CCTTGATCT	TTTCTACGGG	GTCTGACGCT	7560
CAGTGGAACG	AAAACTCACG	TTAAGGGATT	TTGGTCATGA	GATTATCAA	AAGGATCTTC	7620
ACCTAGATCC	TTTTAAATTA	AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	7680
ACTTGGTCTG	ACAGTTACCA	ATGCTTAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	7740
TTTCGTTCAT	CCATAGTTGC	CTGACTCCCC	GTCTGTAGA	TAACTACGAT	ACGGGAGGGC	7800
TTACCATCTG	GCCCCAGTGC	TGCAATGATA	CCGGCAGACC	CACGCTCAC	GGCTCCAGAT	7860
TTATCAGCAA	TAAACCAGCC	AGCCGGAAGG	GCCGAGCGCA	GAAGTGGTCC	TGCAACTTTA	7920
TCCGCCCTCA	TCCAGTCTAT	TAATTGTTGC	CGGGAAAGCTA	GAGTAAGTAG	TTCGCCAGTT	7980
AATAGTTGC	GCAACGTTGT	TGCCATTGCT	ACAGGCATCG	TTGTGTCACG	CTCGTCGTTT	8040
GGTATGGCTT	CATTCAGCTC	CGGTTCCAA	CGATCAAGGC	GAGTTACATG	ATCCCCCATG	8100
TTGTGCAAAA	AAGCGGTTAG	CTCCCTCGGT	CCTCCGATCG	TTGTCAGAAAG	TAAGTTGGCC	8160
GCAGTGTAT	CACTCATGGT	TATGGCAGCA	CTGCATAATT	CTCTTACTGT	CATGCCATCC	8220
GTAAGATGCT	TTTCTGTGAC	TTGTGAGTAC	TCAACCAAGT	CATTCTGAGA	ATAGTGTATG	8280
CGGCGACCGA	GTTGCTCTTG	CCGGCGTCA	ATACGGGATA	ATACCGCGC	ACATAGCAGA	8340
ACTTTAAAAG	TGCTCATCAT	TGGAAAACGT	TCTTCGGGGC	GAAAACCTCTC	AAGGATCTTA	8400
CCGCTGTTGA	GATCCAGTTC	GATGTAACCC	ACTCGTGCAC	CCAACGTAC	TTCAGCATCT	8460
TTTACTTTCA	CCAGCGTTTC	TGGGTGAGCA	AAAACAGGAA	GGCAAAATGC	CGCAAAAAAG	8520
GGAATAAGGG	CGACACGGAA	ATGTTGAATA	CTCATACTCT	TCCTTTTCA	ATATTATTGA	8580
AGCATTATC	AGGGTTATTG	TCTCATGAGC	GGATACATAT	TTGAATGTAT	TTAGAAAAAT	8640
AAACAAATAG	GGGTTCCGCG	CACATTCCC	CGAAAAGTGC	CACCTGACGT	C	8691

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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GACGGATCGG	GAGATCTGCT	AGGTGACCTG	AGGCCGCGCCG	GCTTCGAATA	GCCAGAGTAA	60
CCTTTTTTTT	TAATTTTATT	TTATTTTATT	TTTGAGATGG	AGTTTGGCGC	CGATCTCCG	120
ATCCCCATG	GTGCACTCTC	AGTACAATCT	GCTCTGATGC	CGCATAGTTA	AGCCAGTATC	180
TGCTCCCTGC	TTCGTGTTG	GAGGTGCGTG	AGTAGTGC	GAGCAAATI	TAAGCTACAA	240
CAAGGCAAGG	CTTGACCGAC	AATTGCA	AGAATCTGCT	TAGGGTTAGG	CGTTTTGCGC	300
TGCTTCGCGA	TGTACGGGCC	AGATATA	CGC	TTGACATTG	ATTATTGACT	360
AGTAATCAAT	TACGGGGTCA	TTAGTTCAT	GCCCATATAT	GGAGTTCCGC	GTTACATAAC	420
TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC	CCAAACGACCC	CCGCCCATIG	ACGTCAATAA	480
TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	TGGGTGGACT	540
ATTTACGGTA	AACTGCCAC	TTGGCAGTAC	ATCAAGTGT	TCATATGCCA	AGTACGCC	600
CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATT	TGCCCAGTAC	ATGACCTTAT	660
GGGACTTTCC	TACTTGGCAG	TACATCTACG	TATTAGTCAT	CGCTATTACC	ATGGTGTATGC	720
GGTTTTGGCA	GTACATCAAT	GGGCGTGGAT	AGCGGTTGA	CTCACGGGA	TTTCCAAGTC	780
TCCACCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	GACTTTCAA	840
AATGTGTAA	CAACTCCGCC	CCATTGACGC	AAATGGCGG	TAGGCGTGT	CGGTGGGAGG	900
TCTATATAAG	CAGAGCTCTC	TGGCTAACTA	GAGAACCCAC	TGCTTACTGG	CTTATCGAA	960
TTAATACGAC	TCACATATAGG	GAGACCAAG	CTTGGTACCA	ATTAAATTG	ATATCTCCTT	1020
AGGTCTCGAG	TCTCTAGATA	ACCGGTCAAT	CGATTGGAAT	TCTTGC	GCGCC GCTTGTAGC	1080
CACCATGGAG	TTGTGGTTAA	GCTTGGTCT	TCCTTGTCT	TGTTTTAAAA	GGTGTCCAGT	1140
GTGAAGTGAA	TCTGGTGGAG	TCTGGGGAG	GCTTAGTGCA	GCCTGGAGGG	TCCCTGAAAG	1200
TCTCCTGTGT	AACTCTGGA	TTCACTTTCA	GTGACTATT	CATGTATTGG	GTTCGCCAGA	1260
CTCCAGAGAA	GAGGCTGGAG	TGGGTGCGAT	ACATTAGTCA	AGGTGGTGT	ATAACCGACT	1320
ATCCAGACAC	TGAAAGGGT	CGATTCA	TCTCCAGAGA	CAATGCCAAG	AAACACCTGT	1380
ACCTGCAAAT	GAGCCGCTG	AAAGTCTGAGG	ACACAGCCAT	GTATTACTGT	GCAAGAGGCC	1440
TGGACGACGG	GGCCTGGTTT	GCTTACTGGG	GCCAAGGGAC	TCTGGTCACG	GTCTCTGTAG	1500
CTAGCACCAA	GGGCCCATCG	GTCTTCCCC	TGGCACCC	CTCCAAGAGC	ACCTCTGGGG	1560
GCACAGCGGC	CCTGGCTGC	CTGGTCAAGG	ACTACTCCC	CGAACCGGTG	ACGGTGTGCGT	1620

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GGAACTCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTTCCC	GGCTGTCTTA	CAGTCCTCAG	1680
GACTCTACTC	CCTCAGCAGC	GTGGTCACCG	TGCCCTCCAG	CAGCTGGGC	ACCCAGACCT	1740
ACATCTGCAA	CGTGAATCAC	AAGCCCAGCA	ACACCAAGGT	GGACAAGAAA	GTTGGTGAGA	1800
GGCCAGCACA	GGGAGGGAGG	GTGTCTGCTG	GAAGCCAGGC	TCAGCGCTCC	TGCCTGGACG	1860
CATCCCCGCT	ATGCAGCCCC	AGTCCAGGGC	AGCAAGGCAG	GCCCCGTCTG	CCTCTTCACC	1920
CGGAGGCCTC	TGCCCCGCCCC	ACTCATGCTC	AGGGAGAGGG	TCTTCTGGCT	TTTTCCCCAG	1980
GCTCTGGGCA	GGCACAGGCT	AGGTGCCCT	AACCCAGGCC	CTGCACACAA	AGGGGCAGGT	2040
GCTGGGCTCA	GACCTGCCAA	GAGCCATATC	CGGGAGGGAC	CTGCCCCCTGA	CCTAACGCCA	2100
CCCCAAAGGC	CAAACCTCTCC	ACTCCCTCAG	CTCGGACACC	TTCTCTCCTC	CCAGATTCCA	2160
GTAACTCCCA	ATCTTCTCTC	TGCAGAGCCC	AAATCTTGTG	ACAAAAACTCA	CACATGCCCA	2220
CCGTGCCAG	GTAAGCCAGC	CCAGGCCCTG	CCCTCCAGCT	CAAGGCGGG	CAGGTGCCCT	2280
AGAGTAGCCT	GCATCCAGGG	ACACACCACG	TGGGTACCAA	CATGTCCGG	GCCACATGGA	2340
CAGAGGCCGG	CTCGGCCCCAC	CCTCTGCCCT	GAGAGTGAAC	GCTGTACCAA	CCTCTGTCCC	2400
TACAGGGCAG	CCCCGAGAAC	CACAGGTGTA	CACCCCTGCC	CCATCCCAGG	ATGAGCTGAC	2460
CAAGAACAG	GTCAGCCTGA	CCTGCCTGGT	CAAAGGCTTC	TATCCCAGGG	ACATGCCGT	2520
GGAGTGGGAG	AGCAATGGGC	AGCCGGAGAA	CAACTACAAG	ACCACGCCCTC	CCGTGCTGGA	2580
CTCCGACGGC	TCCCTCTTCC	TCTACAGCA	GCTCACCGTG	GACAAGAGCA	GGTGGCAGCA	2640
GGGGAACGTC	TTCTCATGCT	CCGTGATGCA	TGAGGCTCTG	CACAACCACT	ACACGCAGAA	2700
GAGCCTCTCC	CTGTCTCCGG	GTAAATGAGT	GCGACGGCCG	GCAAGCCCCC	GCTCCCCGGG	2760
CTCTCGGGT	CGCACGAGGA	TGCTTGGCAC	GTACCCCCCTG	TACATACTTC	CCGGGGGCC	2820
AGCATGGAA	TAAAGCACCC	AGCGCTGCC	TGGGGCCCTG	CGAGACTGTG	ATGGTTCTTT	2880
CCACGGGTCA	GGCCGAGTCT	GAGGCCTGAG	TGGCATGAGG	GAGGCAGAGC	GGGTCCCAC	2940
GTCCCCACAC	TGGCCCAGGC	TGTGAGGTG	TGCCTGGGCC	CCCTAGGGTG	GGGCTCAGCC	3000
AGGGGCTGCC	CTCGGCAGGG	TGGGGGATTT	GCCAGCGTGG	CCCTCCCTCC	AGCAGCACCT	3060
GCCCTGGCT	GGGCCACGGG	AAGCCCTAGG	AGCCCTGGG	GACAGACACA	CAGCCCCCTGC	3120
CTCTGTAGGA	GACTGTCTG	TTCTGTGAGC	GCCCCCTGTCC	TCCCGACCTC	CATGCCCACT	3180
CGGGGGCATG	CCTAGTCAT	GTGCGTAGGG	ACAGGCCCTC	CCTCACCCAT	CTACCCCCAC	3240
GGCACTAAC	CCTGGCTGCC	CTGCCAGGC	TCGCACCCGC	ATGGGGACAC	AACCGACTCC	3300
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GCCCAGACCC	GTTCACACAA	CCCCGCACTG	AGGTTGGCCG	GCCACACGGC	CACCACACAC	3420
ACACGTGCAC	GCCTCACACA	CGGAGCCTA	CCCGGGCGAA	CTGCACAGCA	CCCAGACCCAG	3480
AGCAAGGTCC	TCGCACACGT	GAACACTCTC	CGGACACAGG	CCCCCACGAG	CCCCACGCCG	3540
CACCTCAAGG	CCCAAGAGCC	TCTCGGAGC	TTCTCCACAT	GCTGACCTGC	TCAGACAAAC	3600
CCAGCCTCC	TCTCACAAAG	GTGCCCCCTG	AGGCCGCCACA	CACACACAGG	GGATCACACA	3660
CCACGTCACG	TCCCTGGCCC	TGGCCCACCT	CCCAGTGCCG	CCCTTCCCTG	CAGGACGGAT	3720
CAGCCTCGAC	TGTGCTTCT	AGTTGCCAGC	CATCTGTG	TTGCCCCCTCC	CCCGTGCCTT	3780
CCTTGACCCCT	GGAGGTGCC	ACTCCCAC	TCCTTTCTA	ATAAAATGAG	GAAATTGCA	3840
CGCATTGTCT	GAGTAGGTGT	CATTCTATT	TGGGGGGTGG	GGTGGGGCAG	GACAGCAAGG	3900
GGGAGGATTG	GGAAAGACAAT	AGCAGGCATG	CTGGGGATGC	GGTGGGCTCT	ATGGCTTCTG	3960
AGGCAGAAAG	AACCAAGCTGG	GGCTCTAGGG	GGTATCCCCA	CGGCCCTGT	AGCGGGCGCAT	4020
TAAGCGGGC	GGGTGTGGTG	TTACCGCGCA	GCGTGACCGC	TACACTTGCC	AGCGCCCTAG	4080
CGCCCGCTCC	TTTCGCTTTC	TTCCCTTCT	TTCTCGCCAC	GTTCGCCGG	CCTCTCAAAA	4140
AAGGGAAAAA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAT	AGTCCCAGCC	CTAACTCCGC	4200
CCATCCCGCC	CCTAACTCCG	CCCAGTCCG	CCCATTCTCC	GCCCCATGGC	TGACTAATT	4260
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GAGGCTTTT	TGGAGGCC	GGCTTTGCA	AAAAGCTTGG	ACAGCTCAGG	GCTGCATTT	4380
CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	CCCGCTGCCA	4440
TCATGGTCG	ACCATTGAAC	TGCACTGTCG	CCGTGTCCCA	AAATATGGGG	ATTGGCAAGA	4500
ACGGAGACCT	ACCCCTGGCCT	CCGCTCAGGA	ACGAGTTCAA	GTACTTCCAA	AGAATGACCA	4560
CAACCTCTTC	AGTGGAAAGT	AAACAGAAC	TGGTATTAT	GGGTAGGAAA	ACCTGGTTCT	4620
CCATTCTGA	GAAGAACATGA	CCTTTAAAGG	ACAGAAATTAA	TATAGTTCTC	AGTAGAGAAC	4680
TCAAAGAAC	ACCACGAGGA	GCTCATTTC	TTGCCAAAAG	TTTGGATGAT	GCCTTAAGAC	4740
TTATTGAACA	ACCGGAATTG	GCAAGTAAAG	TAGACATGGT	TTGGATAGTC	GGAGGGCAGTT	4800
CTGTTTACCA	GGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTGTG	ACAAGGATCA	4860
TGCAGGAATT	TGAAAGTGCAC	ACGTTTTCC	CAGAAATTGA	TTTGGGGAAA	TATAAAACTTC	4920
TCCCAGAATA	CCCAAGCGTC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	AAGTATAAGT	4980
TTGAAGTCTA	CGAGAAGAAA	GACTAACAGG	AAGATGCTT	CAAGTTCTCT	GCTCCCCCTCC	5040
TAAAGCTATG	CATTTTTATA	AGACCATGGG	ACTTTTGCTG	GCTTTAGATC	TCTTTGTGAA	5100
GGAACCTTAC	TTCTGTGGTG	TGACATAATT	GGACAAACTA	CCTACAGAGA	TTTAAAGCTC	5160
TAAGGTAAT	ATAAAAATT	TAAGTGTATA	ATGTGTTAAA	CTACTGATT	TAATTGTTG	5220

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cont.

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TGAGGAAAAC CTGTTTGCT CAGAAGAAAT GCCATCTAGT GATGATGAGG CTACTGCTGA	5340
CTCTCAACAT TCTACTCCTC CAAAAAAAGAA GAGAAAGGTA GAAGACCCCCA AGGACTTTCC	5400
TTCAGAATTG CTAAGTTTT TGAGTCATGC TGTGTTTAGT AATAGAACCT TTGCTTGCTT	5460
TGCTATTTAC ACCACAAAGG AAAAAGCTGC ACTGCTATAC AAGAAAATTA TGGAAAAATA	5520
TTCTGTAAACC TTTATAAGTA GGCAAAACAG TTATAATCAT AACATACTGT TTTTTCTTAC	5580
TCCACACAGG CATAGAGTGT CTGCTATTA AAACATATGCT CAAAAAATTGT GTACCTTAC	5640
CTTTTTAATT TGAAAGGGG TTAATAAGGA ATATTGATG TATAGTGCCT TGACTAGAGA	5700
TCATAATCAG CCATACCACA TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC	5760
TCCCCCTGAA CCTGAAACAT AAAATGAATG CAATTGTTGT TGTTAACCTTG TTTATTGCAG	5820
CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTT	5880
CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTGGATCG	5940
GCTGGATGAT CCTCCAGCGC GGGGATCTCA TGCTGGAGTT CTTCGCCAC CCCAACCTGT	6000
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC ACAAAATAAG	6060
CATTTTTTC ACTGCATTCT AGTTGTGGT TGTCACAACT CATCAATGTA TCTTATCATG	6120
TCTGTATACC GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTCTG	6180
TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG AGCCGGAAAGC ATAAAGTGT	6240
AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCCTTGCAGC TCACTGCCG	6300
CTTTCAGTC GGGAAACCTG TCGTGCAGC TGCATTAATG ATCGGCCAA CGCGCGGGGA	6360
GAGGCGGTTT CGGTATTGGG CGCTCTTCCG CTTCTCGCT CACTGACTCG CTGCGCTCG	6420
TCGTTGGCT CGGGCGAGCG GTATCAGCTC ACTCAAAGGC GTTAATACGG TTATCCACAG	6480
AATCAGGGGA TAAACGAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC	6540
GTAAAAAGGC CGCGTTGCTG GCGTTTTCC ATAGGCTCCG CCCCCCTGAC GAGCATCACA	6600
AAAATCGACG CTCAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAAGCGT	6660
TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTCCTCGAC CCTGCCGCTT ACCGGATACC	6720
TGTCCGCCCT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGAGGTATC	6780
TCAGTTGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTAGC	6840
CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT	6900
TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGGGAGGTAT GTAGGCGGTG	6960
CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA	7020
TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA	7080
AACAAACAC CGCTGGTAGC GGTGGTTTT TTGTTGCAA GCAGCAGATT ACGCGCAGAA	7140
AAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAAACG	7200
AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAA AAGGATCTTC ACCTAGATCC	7260
TTTAAATTAA AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG	7320
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CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG	7440
GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA	7500
TAAACCAGCC AGCCGGAAGG GCGGAGCGA GAAGTGGTCC TGCAACTTTA TCCGCCCTCCA	7560
TCCAGTCTAT TAATTGTTGC CGGGAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTGC	7620
GCAACGGTGT TGCCATTGCT ACAGGCATCG TGGTGTACG CTCGTCGTTT GGTATGGCTT	7680
CATTCAAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA	7740
AAGCGGTTAG CTCCCTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTAT	7800
CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT	7860
TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA	7920
GTTGCTCTG CCCGGCGTCA ATACGGGATA ATACCGGCC ACATAGCAGA ACTTTAAAG	7980
TGCTCATCAT TGGAAAACGT TCTTCGGGC GAAAACCTCTC AAGGATCTT CCGCTGTTGA	8040
GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTC	8100
CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG	8160
CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTCA ATATTATTGA AGCATTATC	8220
AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTGAAAAAT AAACAAATAG	8280
GGGTTCCCGC CACATTTCCC CGAAAAGTGC CACCTGACGT C	8321

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTACCAATT	TAAATTGATA	TCTCCTTAGG	TCTCGAGCAC	CATGAAGTTG	CCTGTTAGGC	60
TGTTGGTGCT	GATGTTCTGG	ATTCCTGCTT	CCAGCAGTGA	TGTTTGATG	ACCCAAATTC	120
CAGTCTCCCT	GCCTGTCAGT	CTTGGAGATC	AAGCGTCCAT	CTCTTGAGA	TCTAGTCAGA	180
TCATTGTACA	TAATAATGGC	AACACCTATT	TAGAATGGTA	CCTGCAGAAA	CCAGGCCAGT	240
CTCCACAGCT	CCTGATCTAC	AAAGTTCCA	ACCGATTTTC	TGGGGTCCCC	GACAGGTTCA	300
GCGGCAGTGG	ATCAGGGACA	GATTTCACAC	TCAAGATCAG	CAGAGTGGAG	GCTGAGGGATC	360
TGGGAGTTA	TTACTGCTT	CAAGGTTAC	ATGTTCCATT	CACGTTCGGC	TCGGGGACAA	420
AGTTGGAAAT	AAAACGTAAG	TCTCGAGTCT	CTAGATAACC	GGTCAATCGA	TTGGAATTCT	480
AAACTCTGAG	GGGGTCGGAT	GACGTGGCCA	TTCTTGCCT	AAAGCATTGA	GTTTACTGCA	540
AGGTCAGAAA	AGCATGCAA	GCCCTCAGAA	TGGCTGCAA	GAGCTCCAAC	AAAACAATT	600
AGAACTTTAT	TAAGGAATAG	GGGGAAGCTA	GGAAGAAACT	AAAACATCA	AGATTITAAA	660
TACGCTCTT	GGTCTCCITG	CTATAATTAT	CTGGGATAAG	CATGCTGTTT	TCTGTCGTG	720
CCTAACATGC	CCTTATCCGC	AAACAAACACA	CCCAGGGCA	GAACTTGTT	ACTTAAACAC	780
CATCCTGTT	GCTTCTTCC	TCAGGAAC	TGGCTGCACC	ATCTGTC	ATCTTCCCGC	840
CATCTGATGA	GCAGTTGAAA	TCTGGAAC	CCTCTGTTGT	GTGCTGCTG	AATAACTTCT	900
ATCCCAGAGA	GGCCAAAGTA	CAGTGGAGG	TGGATAACGC	CCTCCAATCG	GGTAACCTCC	960
AGGAGAGTGT	CACAGAGCAG	GAGAGCAAGG	ACAGCACCTA	CAGCCTCAGC	AGCACCCCTGA	1020
CGCTGAGCAA	AGCAGACTAC	GAGAAACACA	AAGTCTACGC	CTGCGAAGTC	ACCCATCAGG	1080
GCCTGAGCTC	GCCCGTCACA	AAGAGCTCA	ACAGGGGAGA	GTGTTAGAGG	GAGAAGTGCC	1140
CCCACCTGCT	CCTCAGTTCC	AGCCTGACCC	CCTCCCAC	TTTGGCCTCT	GACCCTTTT	1200
CCACAGGGGA	CCTACCCCTA	TTGCGGTCCT	CCAGCTCATC	TTTCACCTCA	CCCCCTCCCT	1260
CCTCCTTGGC	TTTAATTATG	CTAATGTTGG	AGGAGAATGA	ATAAAATAAG	TGAATCTTTG	1320
CACCTGTGGT	TTCTCTCTT	CCTCATTAA	TAATTATTAT	CTGTTGTTT	ACCAACTACT	1380
CAATTCTCT	TATAAGGAC	AAAATATGTA	GTCATCCTAA	GGCACGTAAC	CATTIATAAA	1440
AATCATCCTT	CATTCTATT	TACCCATCA	TCCTCTGCA	GACAGTCTC	CCTCAAACCC	1500
ACAAGCCTTC	TGTCTCACA	GTCCCCTGGG	CCATGGTAGG	AGAGACTTGC	TTCCTTGT	1560
TCCCCTCCTC	AGCAAGCCCT	CATAGTCCTT	TTTAAGGGTG	ACAGGTCTTA	CAGTCATATA	1620
TCCTTGTGATT	CAATTCCCTG	AGAATCAACC	AAAGCAAATT	TTCAAAAGA	AGAAACCTGC	1680
TATAAAGAGA	ATCATTCTATT	GCAACATGAT	ATAAAAATAAC	AACACAATAA	AAGCAATTAA	1740
ATAAACAAAC	AATAGGGAAA	TGTTTAAGTT	CATCATGGTA	CTTAGACTTA	ATGGAATGTC	1800
ATGCCTTATT	TACATTTTTA	AACAGGTA	GAGGGACTCC	TGTCTGCCA	GGGCCGTATT	1860
GAGTACTTTC	CACAACTCAA	TTTAATCCAC	ACTATACTGT	GAGATTAAAA	ACATTCATTA	1920
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CTTTATTTAC	AAAAGCCAAA	AATTGGAAAT	AGCCGATTG	TCCAACAATA	GAATGAGTTA	2100
TTAAACTGTG	GTATGTTTAT	ACATTAGAAT	ACCCAATGAG	GAGAATTAAC	AAGCTACAAC	2160
TATACCTACT	CACACAGATG	AATCTCATAA	AAATAATGTT	ACATAAGAGA	AACTCAATGC	2220
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TAGAAATTG	GATGGAAATT	ACTCTTAGCT	GGGGGTGGC	GAGTTAGTGC	CTGGGAGAAG	2340
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TGAGTCTGCC	TTCCAGGGCT	CAAGGTGCTC	AAACAAACAA	CAGGCCTGCT	ATTTCTCTGG	2640
CATCTGTGCC	CTGTTTGGCT	AGCTAGGAGC	ACACATACAT	AGAAATTAAA	TGAAACAGAC	2700
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CAAAGGCAGG	CATAATCCAG	TTATGAATT	TTGCGGCCGC	TGCTAGCTT	CACGTGTTGG	3240
ATCCAACCGC	GGAAGGGCCC	TATTCTATAG	TGTCACCTAA	ATGCTAGAGC	TCGCTGATCA	3300

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cont.

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AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC 6960
 ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC 7020
 CCCAGTCTG CAATGATACC GCGAGACCA CGCTCACCGG CTCCAGATT ATCAGCAATA 7080
 AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC 7140
 CAGTCTATT ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC 7200
 AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTGG TATGGCTTCA 7260
 TTCAGCTCCG GTTCCAACG ATCAAGGGCA GTTACATGAT CCCCCATGTT GTGAAAAAAA 7320
 GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAAGAGTA AGTTGGCCGC AGTGTATCA 7380
 CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCCGT AAGATGCTTT 7440
 TCTGTGACTG GTGAGTACTC AACCAAGTC TTCTGAGAAT AGTGTATGCC GCGACCGAGT 7500
 TGCTCTGCC CGCGTCAAT ACGGGATAAT ACCCGGCCAC ATAGCAGAAC TTTAAAAGTG 7560
 CTCATCATTG GAAAAGTTC TTCGGGGCGA AAACCTCTAA GGATCTTACC GCTGTTGAGA 7620
 TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTT TACTTTCAACC 7680
 AGCGTTCTG GGTGAGCAA AACAGGAAGG CAAAATGCCG CAAAAAAAGGG AATAAGGGCG 7740
 ACACGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTATCAG 7800
 GGTTATTGTC TCATGAGCGG ATACATATT GAATGTATTT AGAAAAATAA ACAAAATAGGG 7860
 GTTCCCGCGA CATTTCGGCG AAAAGTGCCA CCTGACGTG ACGGATCGGG AGATCTGCTA 7920
 GCCCGGGTGA CCTGAGGCAC GCGGGCTTCG AATAGCCAGA GTAACCTTT TTTTTAATT 7980
 TATTTTATT ATTGAGTTGAG ATGGAGTTTG GCGCCGATCT CCGATCCCC TATGGTCGAC 8040
 TCTCAGTACA ATCTGCTCTG ATGCCGCATA GTTAAGCCAG TATCTGCTCC CTGCTTGTGT 8100
 GTTGGAGGTC GCTGAGTAGT GCGCGAGCAA AATTAAAGCT ACAAAACAGGC AAGGCTTGAC 8160
 CGACAAATGC ATGAAGAAC TGCCTAGGGT TAGGCGTTTG GCGCTGCTTC GCGATGTACG 8220
 GGCCAGATAT ACCCGTTGAC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG 8280
 GTCATTAGTT CATAGCCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC 8340
 GCCTGGCTGA CGCCCAACG ACCCCCCGGCC ATTGACGTCA ATAATGACGT ATGTTCCCAT 8400
 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GACTATTTAC GGTAAACTGC 8460
 CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTACG CCCCCCTATTG ACGTCAATGA 8520
 CGGTAAATGG CCCGCTGGC ATTATGCCCA GTACATGACC TTATGGGACT TTCCTACTTG 8580
 GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGGGGTTTG GGCAGTACAT 8640
 CAATGGGCCTG GGATAGCGGT TTGACTCACG GGGGTTCCA AGTCTCCACC CCATTGACGT 8700
 CAATGGGAGT TTGTTTGGC ACCAAATCA ACGGGACTTT CCAAAATGTC GTAACAACTC 8760
 CGCCCCATTG ACCCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC 8820
 TCTCTGGCTA ACTAGAGAAC CCACTGCTTA CTGGCTTATC GAAATTAATA CGACTCACTA 8880
 TAGGGAGACC CAAGCTT 8897

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA	60
TTGGAATTCT TCGGGCCGCT TGCTAGCCAC CATGGAGTTG TGGTTAACGT TGGTCTCCT	120
TGTCTTGTT TTAAAAGGTG TCCAGTGTGA AGTGCAGACTG GTGGAGTCTG GGGGAGGCTT	180
AGTGCAGCCT GGAGGGTCCC TGCGACTTT TCCTGCTGCA TCTGGATTCC CGTTCAGTGA	240
CTATTACATG TATTGGGTTC GCCAGGCTCC AGGCAAGGGGA CTGGAGTGGG TCTCATAACAT	300
TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT TCACCATCTC	360
CAGAGACAAT GCAAAGAACA GCCTGTACCT GCAAATGAAC AGCCTGAGGG ACGAGGACAC	420
AGCCGTGTAT TACTGTGCAA GAGGCCTGGC GGACGGGGCC TGGTTGCTT ACTGGGGCCA	480
AGGGACTCTG GTCACGGTCT CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC	540
ACCCCTCTCC AAGAGCACCT CTGGGGCAC AGCGGCCCTG GGCTGCTGG TCAAGGACTA	600
CTTCCCCGAA CCGGTGACGG TGTCTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC	660
CTTCCCCGCT GTCCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TCACCGTGCC	720
CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATACAAGC CCAGCAACAC	780

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CAAGGTGGAC	AAGAAAGTTG	GTGAGAGGCC	AGCACAGGGA	GGGAGGGTGT	CTGCTGGAAG	840
CCAGGCTCAG	CGCTCCTGCC	TGGACGCATC	CGGGCTATGC	AGCCCCAGTC	CAGGGCAGCA	900
AGGCAGGCC	CGTCTGCCTC	TTCACCCGGA	GGCCTCTGCC	CGCCCCACTC	ATGCTCAGGG	960
AGAGGGCTT	CTGGCTTTT	CCCCAGGCTC	TGGGCAGGCA	CAGGCTAGGT	GCCCCTAAC	1020
CAGGCCCTGC	ACACAAAGGG	GCAGGTGCTG	GGCTCAGACC	TGCCAAGAGC	CATATCCGGG	1080
AGGACCTGC	CCCTGACCTA	AGCCCACCCC	AAAGGCCAAA	CTCTCCACTC	CCTCAGCTCG	1140
GACACCTTCT	CTCCCTCCAG	ATTCCAGTAA	CTCCCAATCT	TCTCTCTGCC	GAGCCCAAAT	1200
CTTGTGACAA	AACTCACACA	TGCCCACCGT	GCCCAGGTAA	GCCAGCCCCAG	GCCTCGCCCT	1260
CCAGCTCAAG	GCGGGACAGG	TGCCCTAGAG	TAGCCTGCAT	CCAGGGACAC	ACCACGTGGG	1320
TACCAACATG	TCCGGAGCCA	CATGGACAGA	GGCCGGCTCG	GGCCACCCCTC	TGCCCTGAGA	1380
GTGACCGCTG	TACCAACCTC	TGTCCCTACA	GGGCAGCCCC	GAGAACCCACA	GGTGTACACC	1440
CTGCCCCAT	CCCGGGATGA	GCTGACCAAG	AACCAGGTCA	GCCTGACCTG	CCTGGTCAAA	1500
GGCTTCTATC	CCAGCGACAT	CGCCGTGGAG	TGGGAGAGCA	ATGGGCAGCC	GGAGAACAAAC	1560
TACAAGACCA	CGCCTCCCGT	GCTGGACTCC	GACGGCTCCT	TCTTCCCTCTA	CAGCAAGCTC	1620
ACCGTGGACA	AGAGCAGGTG	GCAGCAGGGG	AACGTCTTCT	CATGCTCCGT	GATGCATGAG	1680
GCTCTGCACA	ACCACTACAC	GCAGAAGAGC	CTCTCCCTGT	CTCCGGGTAA	ATGAGTGCAG	1740
CGGCCGGCAA	GCCCCCGCTC	CCCGGGCTCT	CGCGGTGCGA	CGAGGATGCT	TGGCACGTAC	1800
CCCCTGTACA	TACTTCCCGG	GCGCCAGCA	TGAAAATAAA	GCACCCAGCG	CTGCCCTGGG	1860
CCCCTGCGAG	ACTGTGATGG	TTCTTTCAC	GGGTCAAGGCC	GAGTCTGAGG	CCTGAGTGGC	1920
ATGAGGGAGG	CAGAGCGGGT	CCCACTGTCC	CCACACTGGC	CCAGGCTGTG	CAGGTGTGCC	1980
TGGGCCCTCT	AGGGTGGGGC	TCAGGCCAGGG	GCTGCCCTCG	GCAGGGTGGG	GGATTGCCA	2040
GCGTGGCCCT	CCCTCCAGCA	GCACCTGCC	TGGGCTGGGC	CACGGGAAGC	CCTAGGAGCC	2100
CCTGGGGACA	GACACACAGC	CCCTGCCTCT	GTAGGAGACT	GTCCCTGTTCT	GTGAGCGCCC	2160
CTGTCCTCCC	GACCTCCATG	CCCACCTGGG	GGCATGCCTA	GTCCATGTGC	GTAGGGACAG	2220
GCCCTCCTC	ACCCATCTAC	CCCCACGCA	CTAACCCCTG	GCTGCCCTGC	CCAGCCTCGC	2280
ACCCGCATGG	GGACACAAAC	GAATCCGGGG	ACATGCACTC	TCGGGCCCTG	TGGAGGGACT	2340
GGTGCAGATG	CCACACACAA	CACTCAGCCC	AGACCCGTT	ACAAACCCCC	GCACGTAGGT	2400
TGGCCGGCCA	CACGGCCACC	ACACACACAC	GTGACGCC	CACACACGGA	GCCTCACCCG	2460
GGCGAACTGC	ACAGCACCCA	GACCAAGACA	AGGTCTCGC	ACACGTGAAC	ACTCCTCGGA	2520
CACAGGGCCC	CACGAGCCCC	ACGCGCAC	TCAAGGCCA	CGAGCCTCTC	GGCAGCTTCT	2580
CCACATGCTG	ACCTGCTCAG	ACAAACCCAG	CCCTCCCTCTC	ACAAGGGTGC	CCCTGAGGCC	2640
GCCACACACA	CACAGGGGAT	CACACACCAC	GTCACGTCCC	TGGCCCTGGC	CCACTTCCC	2700
GTGCCGCCCT	TCCCTGCAGG	ACGGATCAGC	CTCGACTGTG	CCTTCTAGTT	CCAGGCCATC	2760
TGTTGTTTG	CCCTCCCGG	TGCCTCCCT	GACCCCTGGAA	GGTGCCTACTC	CCACTGTCCT	2820
TTCTTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCCTGAGT	AGGTGTCTATT	CTATTCTGGG	2880
GGGTGGGGTG	GGGCAGGACA	GCAAGGGGGA	GGATGGGAA	GACAATAGCA	GGCATGCTGG	2940
GGATGGGGTG	GGCTCTATGG	CTTCTGAGGC	GGAAAGAAC	AGCTGGGGCT	CTAGGGGTA	3000
TCCCCACGCG	CCCTGTAGCG	GCGCATTAAG	CGCGCGGGGT	GTGGTGGTTA	CGCGCAGCGT	3060
GACCGCTACA	CTTGCAGCG	CCCTAGCGCC	CGCTCCTTTC	GCTTCTTCTCC	CTTCCTTCT	3120
CGCCACGTT	GGCCGGCCTC	TCAAAAAAAGG	GAAAAAAAGC	ATGCATCTCA	ATTAGTCAGC	3180
AACCATAGTC	CCGCCCCCTAA	CTCCGCCAT	CCCGCCCCCTA	ACTCCGCCA	GTTCCGCCA	3240
TTCTCCGCC	CATGGCTGAC	TAATTTTTTT	TATTATGCA	GAGGCCGAGG	CCGCCTCGGC	3300
CTCTGAGCTA	TTCCAGAAGT	AGTGAGGAGG	CTTTTTGGA	GGCCTAGGCT	TTTGCAAAA	3360
GCTTGGACAG	CTCAGGGCTG	CGATTTCGCG	CCAAACTGTA	CGGCAATCCT	AGCGTGAAGG	3420
CTGGTAGGAT	TTTATCCCCG	CTGCCATCAT	GGTTCGACCA	TTGAACTGCA	TCGTGCCCGT	3480
GTCCTAAAT	ATGGGGATTG	GCAAGAACCG	AGACCTACCC	TGGCCTCCGC	TCAGGAACGA	3540
GTTCAAGTAC	TTCCAAAGAA	TGACCACAAAC	CTCTTCAGTG	GAAGGTAAAC	AGAATCTGGT	3600
GATTATGGGT	AGGAAACCT	GGTTCTCCAT	TCCTGAGAAG	ATCGACCTT	TAAAGGACAG	3660
AATTAATATA	GTTCTCAGTA	GAGAACTCAA	AGAACCCACCA	CGAGGAGCTC	ATTTCTTGC	3720
CAAAAGTTG	GATGATGCCT	TAAGACTTAT	TGAACAACCG	GAATTGGCAA	GTAAAGTAGA	3780
CATGGTTTGG	ATAGTCGGAG	GCAGTTCTGT	TTACCAAGGA	GCCATGAATC	AACCAGGCCA	3840
CCTTAGACTC	TTTGTGACAA	GGATCATGCA	GGAAATTGAA	AGTGACACGT	TTTTCCAGA	3900
AATTGATTTG	GGGAAATATA	AACTTCTCCC	AGAATACCCA	GGCGTCTCT	CTGAGGTCCA	3960
GGAGGAAAAA	GGCATCAAGT	ATAAGTTGA	AGTCTACGAG	AAGAAAGACT	AACAGGAAGA	4020
TGCTTCAAG	TTCTCTGCTC	CCCTCCTAAA	GCTATGCATT	TTTATAAGAC	CATGGGACTT	4080
TTGCTGGCTT	TAGATCTCTT	TGTGAAGGAA	CCTTACTTCT	GTGGTGTGAC	ATAATTGGAC	4140
AAACTACCTA	CAGAGATTAA	AAGCTCTAAG	GTAATATAAA	AATTTTTAAG	TGTATAATGT	4200
GTTAAAATAC	TGATTCTAAAT	TGTTTGTGTA	TTTTAGATTC	CAACCTATGG	AACTGTGAA	4260
TGGGAGCAGT	GGTGAATG	CTTTAATGAG	GAAAACCTGT	TTTGCTCAGA	AGAAATGCCA	4320
TCTAGTGTG	ATGAGGCTAC	TGCTGACTCT	CAACATTCTA	CTCCTCCAAA	AAAGAAGAGA	4380

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AAGGTAGAAG	ACCCCAAGGA	CTTTCCTTCA	GAATTGCTAA	GTTTTTGAG	TCATGCTGTG	4440
TTTAGTAATA	GAACCTCTGC	TTGCTTTGCT	ATTTACACCA	CAAGGAAA	AGCTGCACTG	4500
CTATACAAGA	AAATTATGGA	AAAATATTCT	GTAAACCTTTA	TAATGAGCA	TAACAGTTAT	4560
AATCATAACA	TACTGTTTTT	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	TATTAATAAC	4620
TATGCTAAA	AATTGTGTAC	CTTTAGCTTT	TTAATTGTA	AAGGGTTAA	TAAGGAATAT	4680
TTGATGTATA	GTGCCCTTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTG	TAGAGGTTTT	4740
ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG	AAACATAAAA	TGAATGCAAT	4800
TGTTGTGTT	AACTTGTTTA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	ATAGCATCAC	4860
AAATTCACA	AATAAAGCAT	TTTTTCACT	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	4920
CAATGTATCT	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGGGGG	ATCTCATGCT	4980
GGAGTTCTTC	GCCCCACCCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	AATAAAGCAA	5040
TAGCATCACA	AATTTCACAA	ATAAAGCATT	TTTTCACTG	CATTCTAGTT	GTGGTTGTC	5100
CAAACTCATC	AATGTATCTT	ATCATGTCTG	TATACCGTCG	ACCTCTAGCT	AGAGCTTGGC	5160
GTAATCATGG	TCATAGCTGT	TTCCCTGTGT	AAATTGTTAT	CCGCTCACAA	TTCCACACAA	5220
CATACGAGCC	GGAAAGCATAA	AGTGTAAAGC	CTGGGGTGCC	TAATGAGTG	GCTAACTCAC	5280
ATTAATTGCG	TTGCCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT	GCCAGCTGCA	5340
TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCCT	ATTGGGCGCT	CTTCCGCTTC	5400
CTCGCTCACT	GAETCGCTGC	GCTCGGTCGT	TCGGCTGCGG	CGAGCGGTAT	CAGCTCACTC	5460
AAAGGGCGTA	ATACGGTTAT	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	ACATGTGAGC	5520
AAAAGGCCAG	CAAAGGCCA	GGAACCGTAA	AAAGGCCGCG	TTGCTGGCGT	TTTCCATAG	5580
GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT	GGCGAAACCC	5640
GACAGGACTA	TAAGATACC	AGGCGTTTCC	CCCTGGAAAGC	TCCCTCGTGC	GCTCTCTGT	5700
TCCGACCCCTG	CCGCTTACCG	GATACCTGTC	CGCCTTCTC	CCTTCGGAA	CGTGGCGCT	5760
TTCTCAATGC	TCACGCTGTA	GGTATCTAG	TTCGGTGTAG	GTCGTTGCGT	CCAAGCTGGG	5820
CTGTGTGAC	GAACCCCCCG	TTCAGCCGA	CCGCTGCGCC	TTATCCGGTA	ACTATCGTCT	5880
TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	GTAACAGGAT	5940
TAGCAGAGCG	AGGTATGTAG	GCGGTCTAC	AGAGTTCTTG	AAGTGGTGGC	CTAACTACGG	6000
CTACACTAGA	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	AAGCCAGTTA	CCTTCGGAAA	6060
AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACA	AACCAACCGCT	GGTAGCCGTG	GTTTTTTTGT	6120
TTGCAAGCAG	CAGATTACGC	GCAGAAAAAA	AGGATCTAA	GAAGATCCTT	TGATCTTTTC	6180
TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGTTAA	GGGATTTGG	TCATGAGATT	6240
ATCAAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAAAA	TGAAGTTTTA	AATCAATCTA	6300
AAGTATATAT	GAGTAAACCT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG	AGGCACCTAT	6360
CTCAGCGATC	TGTCTATTTC	GTTCATCCAT	AGTTGCTGTA	CTCCCCGTC	TGTAGATAAC	6420
TACGATACGG	GAGGGCTTAC	CATCTGGCCC	CAGTCTGCA	ATGATACCGC	GAGACCCACG	6480
CTCACCGGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAGGGCCG	AGCGCAGAAG	6540
TGGCTCTGCA	ACTTATACCG	CCTCCATCCA	GTCTATTAAAT	TGTTGCCGGG	AAGCTAGAGT	6600
AAGTAGTTCG	CCAGTTAATA	GTTTGCGBAA	CGTTGTTGCC	ATTGCTACAG	GCATCGGTT	6660
GTCACGCTCG	TGTTTGGTA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	CAAGGCAGT	6720
TACATGATCC	CCCATGTTGT	GCAAAAAGC	GGTTAGCTCC	TCGGTCTCTC	CGATCGTTGT	6780
CAGAAGTAAG	TGAGCCCGCAG	TGTTATCACT	CATGTTATG	GCAGCACTGC	ATAATTCTCT	6840
TAATGTCATG	CCATCCGTA	GATGCTTTTC	TGTGACTGGT	GAGTACTCAA	CCAAGTCATT	6900
CTGAGAATAG	TGTATGCGGC	GACCGAGTTG	CTCTGCCG	GGCTCAATAC	GGGATAATAC	6960
CGCGCCACAT	AGCAGAACCTT	TTAAAGTGCT	CATCATTGGA	AAACGTTCTT	CGGGGCCAAA	7020
ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGTCGATG	TAACCCACTC	GTGCACCCAA	7080
CTGATCTTCA	GCATCTTTTA	CTTTCACCA	CGTTTCTGGG	TGAGCAAAAAA	CAGGAAGGCA	7140
AAATGCCCA	AAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA	TAATCTTCCT	7200
TTTCAATAT	TATTGAAGCA	TTTATCAGGG	TTATTGTC	ATGAGCGGAT	ACATATTGA	7260
ATGTATTTAG	AAAATAAAC	AAATAGGGT	TCCGCGACA	TTTCCCGAA	AAGTGCCACC	7320
TGACGTCGAC	GGATCGGGAG	ATCTGCTAGG	TGACTGAGG	CGCGCCGGCT	TCGAATAGCC	7380
AGAGTAACCT	TTTTTTTTAA	TTTTATTTTA	TTTTATTTTT	GAGATGGAGT	TTGGCGCCGA	7440
TCTCCCGATC	CCCTATGGTC	GACTCTCAGT	ACAATCTGCT	CTGATGCCGC	ATAGTTAAC	7500
CAGTATCTGC	TCCCTGCTTG	TGTGTTGGAG	GTGCGTGTAGT	AGTGCAGCAG	CAAATTTAA	7560
GCTACAACAA	GGCAAGGCTT	GACCGACAAT	TGCATGAAGA	ATCTGCTTAG	GGTTAGGCCT	7620
TTTGCCTG	TTCGCGATGT	ACGGGCCAGA	TATACCGCTT	GACATTGATT	ATTGACTAGT	7680
TATTAATAGT	AATCAATTAC	GGGGTCATTA	TTTCATAGCC	CATATATGGA	GTTCGGCGTT	7740
ACATAACCTA	CGGTAAATGG	CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	CCCATTGACG	7800
TCAATAATGA	CGTATGTTCC	CATAGTAACG	CCAATAGGGA	CTTCCATTG	ACGTCAATGG	7860
GTGGACTATT	TACGGTAAAC	TGCCCACCTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	7920
ACGCCCCCTA	TTGACGTCAA	TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	7980

ACCTTATGGG	ACTTTCTAC	TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	8040
GTGATGCGGT	TTTGGCAGTA	CATCAATGGG	CGTGGATAGC	GTGTTGACTC	ACGGGGATTT	8100
CCAAGTCTCC	ACCCCATTGA	CGTCAATGGG	AGTTTGTGTTT	GGCACCAAA	TCAACGGGAC	8160
TTTCCAAAAT	GTCGTAACAA	CTCCGCCCA	TTGACGCAA	TGGGCGGTAG	GCGTGTACGG	8220
TGGGAGGGTCT	ATATAAGCAG	AGCTCTCTGG	CTAACTAGAG	AACCCACTGC	TTACTGGCTT	8280
ATCGAAATTA	ATACGACTCA	CTATAGGGAG	ACCCAAGCTT	G		8321

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACGGATCGG	GAGATCTGCT	AGCCCGGGTG	ACCTGAGGCG	CGCCGGCTTC	GAATAGCCAG	60
AGTAACCTTT	TTTTTTAATT	TTATTTTATT	TTATTTTGA	GATGGAGTTT	GGCGCCGATC	120
TCCCGATCCC	CTATGGTCGA	CTCTCAGTAC	AATCTGCTCT	GATGCCGCAT	AGTTAACCCA	180
GTATCTGTC	CCTGTTGTG	TGTTGGAGGT	CGCTGAGTAG	TGGCAGAGCA	AAATTTAACG	240
TACAACAAGG	CAAGGCTTGA	CCGACAATTG	CATGAAGAAT	CTGCTTAGGG	TTAGGCCTT	300
TGCGCTGCTT	CGCGATGTAC	GGGCCAGATA	TACCGTTGA	CATTGATTAT	TGACTAGTTA	360
TTAATAGTAA	TCAATTACGG	GGTCATTAGT	TCATAGCCCA	TATATGGAGT	TCCGCGTTAC	420
ATAACTTACG	GTAAATGGCC	CGCCTGGCTG	ACCGCCCAAC	GACCCCGGCC	CATTGACGTC	480
AATAATGACG	TATGTTCCA	TAGTAACGCC	AATAGGGACT	TTCCATTGAC	GTCAATGGGT	540
GGACTATTAA	CGGTAACACTG	CCCACCTGGC	AGTACATCAA	GTGTATCATA	TGCCAAGTAC	600
GCCCCCTATT	GACGTCAATG	ACGGTAATG	GCCCCCCTGG	CATTATGCC	AGTACATGAC	660
CTTATGGGAC	TTTCTACTT	GGCAGTACAT	CTACGTATTA	GTCATCGCTA	TTACCATGGT	720
GATGCGGTTT	TGGCAGTACA	TCAATGGCG	TGGATAGCGG	TTGACTCAC	GGGGATTTC	780
AAGTCTCAC	CCCATTGACC	TCAATGGGAG	TTTGTGTTGG	CACCAAAATC	AACGGGACTT	840
TCCAAAATGT	CGTAACAACT	CCGCCCCATT	GACGCAAATG	GGCGGTAGGC	GTGTACGGTG	900
GGAGGGTCTAT	ATAAGCAGAG	CTCTCTGGCT	AACTAGAGAA	CCCACTGCTT	ACTGGCTTAT	960
CGAAAATTAA	ACGACTCACT	ATAGGGAGAC	CCAAGCTTGG	TACCAATTAA	AATTGATATC	1020
TCCCTTAGGTC	TCGAGCACCA	TGAAGTTGCC	TGTTAGGCTG	TTGGTGTCTGA	TGTTCTGGAT	1080
TCCTGCTTCC	AGCACTGATG	TTGTCTGAC	CCAAACCCCA	CTGTCCAGTC	CTGTCACGCT	1140
TGGACAACCT	GGCTCCCATCT	CTTGCGATC	TAGTCAGATC	ATTGTACATA	ATAATGGCAA	1200
CACCTATCTG	GAATGGTACC	AGCAGAGACC	AGGGCAGTCT	CCACGGCTCC	TGATCTACAA	1260
AGTTTCAAC	CGATTTCTG	GGGTCCCCAGA	CAGGTTCAAG	GGCAGTGGAG	CTGGGACAGA	1320
TTTCACACTC	AAGATCAGCA	GAGTGGAGGC	TGAGGATGTG	GGAGTTTACT	ACTGCTTCCA	1380
GGGTTCACAT	GTTCCTATTCA	CGTTCGGCCA	AGGGACAAAG	TTGAAATCA	AACGTAAGTC	1440
TCGAGTCTCT	AGATAACCGG	TCAATCGATT	CCAATTCTAA	ACTCTGAGGG	GGTCGGATGA	1500
CGTGGCATT	CTTGCCTAA	AGCATTGAGT	TTACTGCAAG	GTCAGAAAAG	CATGCAAAGC	1560
CCTCAGAATG	GCTGCAAAGA	GCTCCAACAA	AAACAATTAG	AACTTTATTA	AGGAATAGGG	1620
GGAAGCTAGG	AAGAAACTCA	AAACATCAAG	ATTTAAATA	CGCTTCTG	TCTCCTGCT	1680
ATAATTATCT	GGGATAAGCA	TGCTGTTTC	TGTCTGCCC	TAACATGCC	TTATCCCAA	1740
ACAACACACC	CAAGGGCAGA	ACTTTGTTAC	TTAACACCCA	TCCTGTTGC	TTCTTCC	1800
AGGAACGTG	GCTGCACCAT	CTGTCCTCAT	CTTCCCGCCA	TCTGATGAGC	AGTTGAATC	1860
TGGAACGTCC	TCTGTTGTG	GCCTGCTGA	TAACCTCTAT	CCCAGAGAGG	CCAAAGTACA	1920
GTGGAAGGTG	GATAACGCC	TCCAATCGGG	TAACCTCCAG	GAGAGTGTCA	CAGAGCAGGA	1980
GAGCAAGGAC	AGCACCTACA	GCCTCAGCAG	CACCTGACG	CTGAGCAAAG	CAGACTACGA	2040
GAAACACAAA	GTCTACGCC	GCGAAGTCAC	CCATCAGGGC	CTGAGCTCGC	CCGTACACAA	2100
GAGCTTCAAC	AGGGGAGAGT	GTTAGAGGGA	GAAGTGC	CCACCTGCTCC	TCAGTTCCAG	2160
CCTGACCCCC	TCCCATCCTT	TGGCCTCTGA	CCCTTTTCC	ACAGGGGACC	TACCCCTATT	2220
GCGGTCTCC	AGCTCATCTT	TCACCTCACC	CCCCTCCTCC	TCCTTGGCTT	TAATTATGCT	2280
AATGTTGGAG	GAGAATGAAT	AAATAAAGTG	AATCTTGCA	CCTGTGGTTT	CTCTCTTCC	2340
TCATTTAATA	ATTATTATCT	GTTGTTTAC	CAACTACTCA	ATTCTCTTA	TAAGGGACTA	2400
AATATGTAGT	CATCCTAAGG	CACGTAACCA	TTTATAAAA	TCATCCTCA	TTCTATT	2460

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CCCTATCATC	CTCTGCAAGA	CAGTCCTCCC	TCAAACCCAC	AAGCCTTCTG	TCCTCACAGT	2520
CCCCTGGGCC	ATGGTAGGAG	AGACTTGTT	CCTTGTTTC	CCCTCCTCAG	CAAGCCCTCA	2580
TAGTCCTTTT	TAAGGGTGAC	AGGTCTTACA	GTCATATATC	CTTGATTCA	ATTCCTGAG	2640
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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAGAGGAAG ACTGACGGTG CCCCCGCGAG TTCAGGTGCT GAGG

44

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCAGCACCC TGAACTCGCG GGGGCACCGT CAGTCTTCCT CTTC

44

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGGGAGGGC TTTGTTGGAG ACCGAGCACG AGTACGACTT GCCATTCAAGC C

51

B
cont.
(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATGGTTTTC TCGATGGCGG CTGGGAGGGC

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCCTCCCAG CCGCCATCGA GAAAACCATC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGTTTTC TCGATAGCGG CTGGGAGGGC TTTG

34

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATGGTTTTC TCGATGGCGG CTGGGAGGGC TTTGTTGGAG ACCGAGCACG AGTACGACTT
GCCATTCAAGC CAGTCCTGGT G

60

81

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACCAGGACT GGCTGAATGG CAAGTCGTAC TCGTGCTCGG TCTCCAACAA AGCCCTCCCC
GCCGCCATCG AGAAAACCAT C

60

81

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA
TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG TGGTTAACGCT TGGTCTTCCT
TGTCTTGTT TTAAAAGGTG TCCAGTGTGA AGTGCACACTG GTGGAGTCTG GGGGAGGCTT
AGTGCAGCCT GGAGGGTCCC TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCACTGA
CTATTACATG TATTGGGTTC GCCAGGCTCC AGGCAAGGGGA CTGGAGTGGG TCTCATAACAT

60

120

180

240

300

6
unf.

TAGTCAAGAT	GGTGATATAA	CCGACTATGC	AGACTCCGTA	AAGGGTCGAT	TCACCACCTC	360
CAGAGACAAT	GCAAAGAAC	GCCTGTACCT	GCAAATGAAC	AGCCTGAGGG	ACGAGGACAC	420
AGCGTGTAT	TACTGTCAA	GAGGCCTGGC	GGACGGGGCC	TGGTTTGCTT	ACTGGGGCCA	480
AGGGACTCTG	GTCACGGTCT	CTTCCGCTAG	CACCAAGGGC	CCATCGGTCT	TCCCCCTGGC	540
ACCCCTCTCC	AAGAGCACCT	CTGGGGGCAC	AGCGGCCCTG	GGCTGCTGG	TCAAGGACTA	600
CTTCCCCGAA	CCGGTGACGG	TGTCGTGAA	CTCAGGCGCC	CTGACCAGCG	GCGTGCACAC	660
CTTCCCCGCT	GTCCTACAGT	CCTCAGGACT	CTACTCCCTC	AGCAGCGTGG	TCACCGTGCC	720
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CAAGGTGGAC	AAGAAAGTTG	GTGAGAGGCC	AGCACAGGGA	GGGAGGGTGT	CTGCTGGAAG	840
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CCCTGCAGCC	GCCACACACA	CACAGGGAT	CACACACCAC	GTCACGCTCC	TGGCCCTGGC	3060
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B
cont.

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AGCTGCACTG	CTATACAAAGA	AAATTATGGA	AAAATATTCT	GTAAACCTTA	TAAGTAGGCA	4920
TAACAGTTAT	AATCATAACA	TACTGTTTT	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	4980
TATTAATAAC	TATGCTAAA	AATTGTTGAC	CTTCTAGCTT	TTAATTGTA	AAGGGGTTAA	5040
TAAGGAATAT	TTGATGTATA	GTGCCTTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTG	5100
TAGAGGTTT	ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG	AAACATAAAA	5160
TGAATGCAAT	TGTTGTTGTT	AACTTGTAA	TTGCAGCTTA	TAATGGTTAC	AAATAAAGCA	5220
ATAGCATCAC	AAATTTACA	AATAAAGCAT	TTTTTCACT	GCATTCTAGT	TGTGGTTTGT	5280
CCAAACTCAT	CAATGTATCT	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGCGGG	5340
ATCTCATGCT	GGAGTTCTTC	GCCCCCCCCA	ACTTGTTTAT	TGCACTTAT	AATGGTTACA	5400
AATAAAAGCAA	TAGCATCACA	AAATTCAAA	ATAAAGCATT	TTTTTCACTG	CATTCTAGTT	5460
GTGGTTGTC	CAAACTCATC	AATGTATCTT	ATCATGTCTG	TATACCGTCG	ACCTCTAGCT	5520
AGAGCTTGGC	GTAATCATGG	TCATAGCTGT	TTCTGTGTC	AAATTGTTAT	CCGCTCACAA	5580
TTCCACACAA	CATACGAGCC	GGAAAGCATAA	AGTGTAAAGC	CTGGGGTGCC	TAATGAGTGA	5640
GCTAACTCAC	ATTAATTGCG	TTGCGCTAC	TGCCCCCTTT	CCAGTCGGGA	AACCTGTCGT	5700
GCCAGCTGCA	TTAATGAATC	GGCCAACCGG	CGGGGAGAGG	CGGTTGCGT	ATTGGCGCT	5760
CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTGCGT	TGCGCTGCGG	CGAGCGGTAT	5820
CAGCTCACTC	AAAGGCGGT	ATACGGTTAT	CCACAGAATC	AGGGGATAAC	GCAGGAAAGA	5880
ACATGTGAGC	AAAAGGCCAG	CAAAAGGCCA	GGAAACCGTAA	AAAGGGCGCG	TTGCTGGCGT	5940
TTTCCATAG	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT	6000
GGCGAAACCC	GACAGGACTA	TAAGATACC	AGGCCTTCC	CCCTGGAAGC	TCCCTCGTGC	6060
GCTCTCTGT	TCCGACCCCTG	CCGCTTACCG	GATACTGTGTC	CGCCTTTCTC	CCTTCGGGAA	6120
GCGTGGCGCT	TTCTCAATGC	TCACGCTGTA	GGTATCTCAG	TTCGGTGTAG	GTCGTTCGCT	6180
CCAAGCTGGG	CTGTGTGCAC	GAACCCCCCG	TTCACTGCGA	CCGCTGCGCC	TTATCCGGTA	6240
ACTATCGTCT	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	6300
GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AAGTGGTGGC	6360
CTAACTACGG	CTACACTAGA	AGGACAGTAT	TTGGTATCTG	CGCTCTGCTG	AAGCCAGTTA	6420
CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT	CCGGCAAACAA	AACCACCGCT	GGTAGCGGTG	6480
GTTTTTTGT	TTGCAAGCAG	CAGATTACGC	GCAGAAAAAA	AGGATCTAA	GAAGATCCTT	6540
TGATCTTTC	TACGGGGTCT	GACGCTCACT	GGAAACGAAA	CTCACGTTAA	GGGATTTTGG	6600
TCATGAGATT	ATCAAAAGG	ATCTTCACCT	AGATCCTTTT	AAATTAAAAA	TGAAGTTTTA	6660
AATCAATCTA	AAGTATATAT	GAGTAAACTT	GGTCTGACAG	TTACCAATGC	TTAATCAGTG	6720
AGGCACCTAT	CTCAGCGATC	TGTCTATTTC	GTTCATCCAT	AGTTGCCTGA	CTCCCCGTG	6780
TGTAGATAAC	TACGATACGG	GAGGGCTTAC	CATCTGGCCC	CAGTGTGCA	ATGATAACCGC	6840
GAGACCCACG	CTCACCGGCT	CCAGATTAT	CAGCAATAAA	CCAGCCAGCC	GGAAAGGGCCG	6900
AGCGCAGAAG	TGGCCTGCA	ACTTTATCCG	CCTCCATCCA	GTCTATTAAAT	TGTTGCCGGG	6960
AAGCTAGAGT	AAGTAGTTCG	CCAGTTAATA	GTGGCGCAA	CGTTGTTGCC	ATTGCTACAG	7020
GCATCGGGT	GTCACGCTCG	TCGTTTGGTA	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	7080
CAAGGGAGT	TACATGATCC	CCCATGTTGT	GCAAAAAAAGC	GGTTAGCTCC	TTCGGTCCCTC	7140
CGATCGTTGT	CAGAAGTAAG	TTGGCCGAG	TGTTATCACT	CATGGTTATG	GCAGCACTGC	7200
ATAATTCTCT	TACTGTATG	CCATCCGTA	GATGCTTTTC	TGTGACTGGT	GAGTACTCAA	7260
CCAAGTCATT	CTGAGAAATAG	TGTATGCCG	GACCGAGTTG	CTCTTGCCCG	GGTCAATAC	7320
GGGATAATAC	CGCGCCACAT	AGCAGAACTT	TAAAAGTGCT	CATCATTGGA	AAACGTTCTT	7380
CGGGGGCGAA	ACTCTCAAGG	ATCTTACCGC	TGTTGAGATC	CAGTCGATG	TAACCCACTC	7440
GTGCACCCAA	CTGATCTTCA	GCATCTTTA	CTTCACCAAG	CGTTTCTGGG	TGAGCAAAAA	7500

CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT	TGAATACTCA	7560
TAATCTTCTT	TTTCATAATAT	TATTGAAGCA	TTTATCAGGG	TTATTGTCTC	ATGAGCGGAT	7620
ACATATTGAA	ATGTATTTAG	AAAATAAAC	AAATAGGGT	TCCGCGCACA	TTTCCCCGAA	7680
AAGTGCCACC	TGACGTCGAC	GGATCGGGAG	ATCTGCTAGG	TGACCTGAGG	CGCGCCGGCT	7740
TCGAATAGCC	AGAGTAACCT	TTTTTTTTAA	TTTTATTTA	TTTTATTTT	GAGATGGAGT	7800
TTGGCGCCGA	TCTCCCGATC	CCCTATGGTC	GACTCTCAGT	ACAATCTGCT	CTGATGCCGC	7860
ATAGTTAACG	CAGTATCTGC	TCCCTGCTTG	TGTGTTGGAG	GTCGCTGAGT	AGTGCGCGAG	7920
CAAATTTAA	GCTACAACAA	GGCAAGGCTT	GACCGACAAT	TGCATGAAGA	ATCTGCTTAG	7980
GGTTAGGCCT	TTTGCCTGTC	TTCGCGATGT	ACGGGCCAGA	TATAACGCGTT	GACATTGATT	8040
ATTGACTAGT	TATTAATAGT	AATCAATTAC	GGGGTCATTA	TTTCATAGCC	CATATATGGA	8100
GTTCCCGCTT	ACATAACTTA	CGGTAAATGG	CCCAGCCTGGC	TGACCGCCCCA	ACGACCCCCG	8160
CCCATTGACG	TCAATAATGA	CGTATGTTCC	CATAGTAACG	CCAATAGGG	CTTTCCATTG	8220
ACGTCAATGG	GTGGACTATT	TACGGTAAAC	TGCCCCACTTG	GCAGTACATC	AAGTGTATCA	8280
TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	8340
CCAGTACATG	ACCTTATGGG	ACTTTCTAC	TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	8400
TATTACCATG	GTGATGCGGT	TTTGGCAGTA	CATCAATGGG	CCTGGATAGC	GGTTGACTC	8460
ACGGGGATTT	CCAAGTCTCC	ACCCCATGTA	CGTCAATGGG	AGTTTGTTTT	GGCACCAAAA	8520
TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA	CTCCGCCCCA	TTGACGCAA	TGGGCGGTAG	8580
GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	AGCTCTCTGG	CTAACTAGAG	AACCCACTGC	8640
TTACTGGCTT	ATCGAAATTA	ATACGACTCA	CTATAGGGAG	ACCCAAGCTT		8690

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTACCAATT	TAAATTGATA	TCTCCTTCTAGG	TCTCGAGTCT	CTAGATAACC	GGTCAATCGA	60
TTGGAATTCT	TGCGGCCGCT	TGCTAGCACC	AAGGGCCCAT	CGGTCTTCCC	CCTGGCACCC	120
TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG	GCCCTGGGCT	GCCTGGTCAA	GGACTACTTC	180
CCCGAACCGG	TGACGGTGTGTC	GTGGAACCTCA	GGCCTCCCTGA	CCAGCGGGGT	GCACACCTTC	240
CCGGCTGTCC	TACAGTCCTC	AGGACTCTAC	TCCCTCAGCA	GCGTGGTCAAC	CGTGCCCTCC	300
AGCAGCTTGG	GCACCCAGAC	CTACATCTGC	AACGTGAATC	ACAAGCCCAG	CAACACCAAG	360
GTGGACAAAGA	AAAGTTGGTGA	GAGGCCAGCA	CAGGGAGGG	GGGTGTCTGC	TGGAAGCCAG	420
GCTCAGCGCT	CCTGCCCTGGA	CGCATCCCGG	CTATGCAGCC	CCAGTCCAGG	GCAGCAAGGC	480
AGGCCCCGTC	TGCCCTCTTC	CCCGGAGGCC	TCTGCCCGCC	CCACTCATGC	TCAGGGAGAG	540
GGTCTTCTGG	CTTTTTCCCCC	AGGCTCTGGG	CAGGCACAGG	CTAGGTGCC	CTAACCCAGG	600
CCCTGCACAC	AAAGGGGCAG	GTGCTGGGCT	CAGACCTGCC	AAGAGCCATA	TCCGGGAGGA	660
CCCTGCCCT	GACCTAAGCC	CACCCAAAG	GCCAAACTCT	CCACTCCCTC	AGCTCGGACA	720
CCTTCTCTCC	TCCCAGATTC	CAGTAACTCC	CAATCTTCTC	TCTGCAGAGC	CCAAATCTTG	780
TGACAAAAC	CAACACATGCC	CACCGTCCCC	AGGTAAGCCA	GCCCAGGCC	CGCCCTCCAG	840
CTCAAGCGG	GACAGGTGCC	CTAGAGTAGC	CTGCATCCAG	GGACAGGCC	CAGCCGGGTG	900
CTGACACGTC	CACCTCCATC	TCTTCTCTAG	CACCTGAAC	CCTGGGGGGA	CCGTCAGTCT	960
TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CGGGACCCCT	GAGGTACAT	1020
GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	TACGTGGACG	1080
GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCAGGGAGGA	GCAGTACAAC	AGCACGTACC	1140
GTGTGGTCAG	CGTCCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	GAGTACAAGT	1200
GCAAGGTCTC	CAACAAAGCC	CTCCAGGCC	CCATCGAGAA	AACCATCTCC	AAAGCCAAAG	1260
GTGGGACCCG	TGGGGTGCAG	GGGCCACATG	GACAGAGGCC	GGCTCGGCC	ACCCCTCTGCC	1320
CTGAGAGTGA	CCGCTGTACC	AACCTCTGTC	CCTACAGGGC	AGCCCCGAGA	ACCACAGGTG	1380
TACACCCCTGC	CCCCATCCCG	GGATGAGCTG	ACCAAGAAC	AGGTCAAGCCT	GACCTGCC	1440
GTCAAAGGCT	TCTATCCCAG	CGACATGCC	GTGGAGTGGG	AGAGCAATGG	GCAGCCGGAG	1500
AACAACATACA	AGACCACGCC	TCCCGTGTG	GACTCCGACG	GCTCTTCTT	CCTCTACAGC	1560
AAGCTCACCG	TGGACAAGAG	CAGGTGGCAG	CAGGGGAACG	TCTTCTCATG	CTCCGTGATG	1620

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cont.

CATGAGGCTC	TGCACAACCA	CTACACGCAG	AAGAGCCTCT	CCCTGTCTCC	GGGTAAATGA	1680
GTGCGACGGC	CGGCAAGCCC	CCGCTCCCCG	GGCTCTCGCG	GTCGCACGAG	GATGCTTGGC	1740
ACGTACCCCC	TGTACATACT	TCCCAGGCGC	CCAGCATGGA	AATAAAGCAC	CCAGCGCTGC	1800
CCTGGGCCCC	TGCGAGACTG	TGATGGTTCT	TTCCACGGGT	CAGGCCGAGT	CTGAGGCCCTG	1860
AGTGGCATGA	GGGAGGCAGA	GCGGGTCCA	CTGCCCCAC	ACTGGCCCAG	GCTGTGCAGG	1920
TGTGCGCTGG	CCCCCTAGGG	TGGGGCTCAG	CCAGGGGCTG	CCCTCGGCAG	GGTGGGGGAT	1980
TTGCCAAGCGT	GGCCCTCCCT	CCAGCAGCAC	CTGCCCTGGG	CTGGGCCACG	GGAAGCCCTA	2040
GGAGCCCCCTG	GGGACAGACA	CACAGCCCT	GCCTCTGTAG	GAGACTGTCC	TGTTCTGTGA	2100
GCGCCCCCTGT	CCTCCCGACC	TCCATGCCA	CTCGGGGCA	TGCTGGGGAT	GCGGTGGGCT	2160
CTATGGCTTC	TGAGGCGGAA	AGAACAGCT	GGGGCTCTAG	GGGGTATCCC	CACGCGCCCT	2220
GTAGCGCGC	ATTAAGCGCG	GCGGGTGTGG	TGGTTACGCG	CAGCGTGACC	GCTACACATTG	2280
CCAGCGCCCT	AGCGCCCGCT	CCTTTCGCTT	TCTTCCCTTC	CTTCTCGCC	ACGTTCGCCG	2340
GCTTCCCCG	TCAAGCTCTA	AATCGGGCA	TCCCTTCTAGG	GTTCCGATT	AGTGCCTTAC	2400
GGCACCTCGA	CCCCAAAAAA	CTTGATTTAGG	GTGATGGTTC	ACGTAGTGGG	CCATCGCCCT	2460
GATAGACGGT	TTTCGCCCC	TTGACGTTGG	AGTCACAGTT	CTTTAATAGT	GGACTCTTGT	2520
TCCAAACTGG	AACAACACTC	AACCTATCT	CGGTCTATTTC	TTTGATTTA	TAAGGGATTT	2580
TGGGGATTTG	GGCCTATTGG	TTAAAAAATG	AGCTGATTTA	ACAAAAAATT	AACGCGAATT	2640
AATTCTGTGG	AATGTGTGTC	AGTTAGGGT	TGGAAAGTCC	CCAGGCTCCC	CAGGCAGGCA	2700
GAAGTATGCA	AAGCATGCA	CTCAATTAGT	CAGCAACCAT	AGTCCCGCCC	CTAACTCCGC	2760
CCATCCCGCC	CCTAACTCCG	CCCAGTTCCG	CCCATTCTCC	GCCCCATGGC	TGACTAATTT	2820
TTTTTATTTA	TGCAAGAGGCC	GAGGCCGCT	CGGCCTCTGA	GCTATTCCAG	AAGTAGTGAG	2880
GAGGCTTTTT	TGGAGGCCA	GGCTTTGCA	AAAAGCTTGG	ACAGCTCAGG	GCTGCGATTT	2940
CGCGCCAAAC	TTGACGGCAA	TCCTAGCGTG	AAGGCTGGTA	GGATTTTATC	CCCGCTGCCA	3000
TCATGGTTCG	ACCATTGAAC	TGCATCGTC	CCGTGTCCCA	AAATATGGGG	ATTGGCAAGA	3060
ACGGAGACCT	ACCCCTGGCCT	CCGCTCAGGA	ACGAGTTCAA	GTACTTCCAA	AGAATGACCA	3120
CAACCTCTTC	AGTGGAGGT	AAACAGAACAT	TGGTGTATTAT	GGGTAGGAAA	ACCTGGTTCT	3180
CCATTCTGTA	GAAGAACATCGA	CCTTTAAAGG	ACAGAAATTAA	TATAGTTCTC	AGTAGAGAAC	3240
TCAAAGAACC	ACCACGAGGA	GCTCATTTTC	TTGCCAAAAG	TTTGGATGAT	GCCTTAAGAC	3300
TTATTGAACA	ACCGGAATTG	GCAAGTAAG	TAGACATGGT	TTGGATAGTC	GGAGGCAGTT	3360
CTGTTTACCA	GGAAAGCCATG	AATCAACCG	GCCACCTTAG	ACTCTTGTG	ACAAGGATCA	3420
TGCGAGGATT	TGAAAGTGCAC	ACGTTTTTC	CAGAAATTGA	TTTGGGGAAA	TATAAACTTC	3480
TCCCAGAATA	CCCAGGCCTC	CTCTCTGAGG	TCCAGGAGGA	AAAAGGCATC	AAGTATAAGT	3540
TTGAAGCTCA	CGAGAAGAAA	GACTAACAGG	AAGATGCTTT	CAAGTTCTCT	GCTCCCTCC	3600
TAAAGCTATG	CATTTTTATA	AGACCATGGG	ACTTTTGCTG	GCTTTAGATC	TCTTTGTGAA	3660
GGAACCTTAC	TTCTGTGGTG	TGACATAATT	GGACAAACTA	CCTACAGAGA	TTTAAAGCTC	3720
TAAGGTAAT	ATAAAATTTT	TAAGTGTATA	ATGTGTTAAA	CTACTGATTCT	TAATTGTTG	3780
TGTATTTTAG	ATTCCAACCT	ATGGAACATG	TGAATGGGAG	CAGTGGTGG	ATGCCTTTAA	3840
TGAGGAAAAC	CTGTTTGTGCT	CAGAAGAAAT	GCCATCTAGT	GATGATGAGG	CTACTGCTGA	3900
CTCTCAACAT	TCTACTCCCTC	CAAAAAAGAA	GAGAAAGGTA	GAAGACCCCCA	AGGACTTTCC	3960
TTCAGAATTG	CTAAGTTTTT	TGAGTCATGC	TGTGTTAGT	AATAGAAACTC	TTGCTTGCTT	4020
TGCTATTAC	ACCCACAAAGG	AAAAGCTGC	ACTGCTATAC	AAGAAAATT	TGGAAAATA	4080
TTCTGTAAACC	TTTATAAGTA	GGCATAACAG	TTATAATCAT	ACACATACTGT	TTTTCTTAC	4140
TCCACACAGG	CATAGACTGT	CTGCTATTAA	TAACTATGCT	CAAAAATTGT	GTACCTTAC	4200
CTTTTAATT	TGTAAAGGGG	TAAATAAGGA	ATATTGATG	TATAGTGCCT	TGACTAGAGA	4260
TCATAATCAG	CCATACCCACA	TTTGAGGAG	TTTACTTGC	TTTAAAAAAC	CTCCACACCC	4320
TCCCCCTGAA	CCTGAAACAT	AAAATGAATG	CAATTGTTGT	TGTTAACTTG	TTTATTGCAG	4380
CTTATAATGG	TTACAAATAA	AGCAATAGCA	TCACAAATT	CACAAATAAA	GCATTTTTT	4440
CACTGCATTC	TAGTTGTGGT	TTGTCCAAAC	TCATCAATGT	ATCTTATCAT	GTCTGGATCG	4500
GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	TGCTGGAGTT	CTTCGCCAC	CCCAACTTGT	4560
TTATTGCGAC	TTATAATGGT	TACAAATAA	GCAATAGCAT	CACAAATTTC	ACAAATAAG	4620
CATTTTTTC	ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG	4680
TCTGTATACC	GTCGACCTCT	AGCTAGAGCT	TGGGTAATC	ATGGTCATAG	CTGTTCTCG	4740
TGTGAAATTG	TTATCGCCTC	ACAATTCCAC	ACAAACATACG	AGCCGGAAGC	ATAAAGTGT	4800
AAGCCTGGGG	TGCTTAATGA	GTGAGCTAAC	TCACATTAA	TGCGTTGCGC	TCACTGCCG	4860
CTTTCAGTC	GGGAAACCTG	TCGTGCCAGC	TGCATTAATG	AATCGGCCAA	CGCGGGGGA	4920
GAGGCGGTTT	GGCTATTGGG	CGCTCTTCG	CTTCTCGCT	CACTGACTCG	CTGCGCTCG	4980
TCGTTCGGCT	GCGCGAGCG	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	TTATCCACAG	5040
AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGCAAAGG	CCAGCAAAG	GCCAGGAACC	5100
GTAAAAAGGC	CGCGTTGCTG	GCGTTTTCC	ATAGGCTCCG	CCCCCTGAC	GAGCATCACA	5160
AAAATCGACG	CTCAAGTCAG	AGGTGGCAGA	ACCCGACAGG	ACTATAAAGA	TACCAGGCCT	5220

TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC 5280
 TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGTTAGGTATC 5340
 TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC 5400
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 TATGCCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT GTAGGCGGTG 5520
 CTACAGAGTT CTTGAAGTGG TGGCCTAATC ACGGCTACAC TAGAAGGACA GTATTGGTA 5580
 TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA 5640
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 AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAA AAGGATCTTC ACCTAGATCC 5820
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 ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTCAT 5940
 CCATAGTTGC CTGACTCCCC GTCGTGTTAG TAATCTACGAT ACGGGAGGGC TTACCATCTG 6000
 GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA 6060
 TAAACCAGCC AGCCGGAAGG GCGGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA 6120
 TCCAGTCTAT TAAATTGTTGC CGGGGAAGCTA GAGTAAGTAG TTGCCCAGTT AATAGTTGC 6180
 GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTACAG CTCGTCGTTT GGTATGGCTT 6240
 CATTCACTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA 6300
 AAGCGGTTAG CTCCCTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTAT 6360
 CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT 6420
 TTTCTGTGAC TGGTGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA 6480
 GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG 6540
 TGCTCATCAT TGAAAACGT TCTTCGGGCG GAAAACCTCTC AAGGATCTTA CCGCTGTTGA 6600
 GATCCAGTTC GATGTAACCC ACTCGTGAC CCAACTGATC TTCAGCATCT TTTACTTTCA 6660
 CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAAG GGAATAAAGGG 6720
 CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTCA ATATTATTGA AGCATTATTC 6780
 AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG 6840
 GGGTTCCCGCG CACATTTCCT CGAAAAGTGC CACCTGACGT CGACGGATCG GGAGATCTGC 6900
 TAGGTGACCT GAGGCGCGCC GGCTTCGAAT AGCCAGAGTA ACCTTTTTTT TTAATTTTAT 6960
 TTTATTTTAT TTTTGAGATG GAGTTTGGCG CCGATCTCCC GATCCCCCTAT GGTCGACTCT 7020
 CAGTACAATC TGCTCTGATG CCGCATAGT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT 7080
 GGAGGTCGCT GAGTAGTGC CGAGCAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA 7140
 CAATTGATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC 7200
 CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC 7260
 ATTAGTTCAT AGCCCATATA TGGAGTTCGG CGTTACATAA CTTACGGTAA ATGGCCCGCC 7320
 TGGCTGACCG CCCAACGACC CCCGCCATT GACGTCATAA ATGACGTATG TTCCCATAGT 7380
 AACGCCATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT AAAACTGCCA 7440
 CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCC CCTATTGACG TCAATGACGG 7500
 TAAATGGCCC GCCTGGCATT ATGCCCAAGTA CATGACCTTA TGGGACTTTTC CTACTTGGCA 7560
 GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGTATG CGGTTTTGGC AGTACATCAA 7620
 TGGGCGTGGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA 7680
 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC 7740
 CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGGTGGAG GTCTATATAA GCAGAGCTCT 7800
 CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG 7860
 GGAGACCCAA GCTT 7874

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Ley	Val	Gln	Pro	Gly	Gly	
1															
10															
15															
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Pro	Phe	Ser	Asp	Tyr

20	25	30	
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly	Leu Glu Trp Val		
35	40	45	
Ser Tyr Ile Ser Gln Asp Gly Asp Ile Thr Asp Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Gly Leu Ala Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly			
100	105	110	
Thr Leu Val Thr Val Ser Ser			
115			

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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unx .

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys			
1	5	10	15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr			
20	25	30	
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser			
35	40	45	
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser			
50	55	60	
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr			
65	70	75	80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys			
85	90	95	
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys			
100	105	110	
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro			
115	120	125	
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys			
130	135	140	
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp			
145	150	155	160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu			
165	170	175	
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu			
180	185	190	
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Asp Lys Val Ser Asn			
195	200	205	
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly			
210	215	220	
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu			
225	230	235	240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr			
245	250	255	
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn			
260	265	270	

Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
					275			280				285			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
					290			295			300				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
					305			310			315			320	
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
					325			330							

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1					5				10				15		
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
					20				25				30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
					35				40				45		
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
					50				55				60		
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
					65				70				75		80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
					85				90				95		
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
					100				105				110		
Pro	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
					115				120				125		
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
					130				135				140		
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
					145				150				155		160
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
					165				170				175		
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
					180				185				190		
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
					195				200				205		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
					210				215				220		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Val Asn Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Lys Val Ser Cys Val Thr Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Tyr Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Tyr Ile Ser Gln Gly Gly Asp Ile Thr Asp Tyr Pro Asp Thr Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Ser Arg Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Gly Leu Asp Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Val Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220
Thr His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val
225 230 235 240
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
245 250 255
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
260 265 270
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
275 280 285
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
290 295 300
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
305 310 315 320
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
325 330 335
Pro Gly Lys

B
wrd.